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Terms	Documents
HSP70 same arthritis	10

**Database:**

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US Pre-Grant Publication Full-Text Database  
JPO Abstracts Database  
EPO Abstracts Database  
Derwent World Patents Index  
IBM Technical Disclosure Bulletins

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L14

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<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=OR</i>			
<u>L14</u>	HSP70 same arthritis	10	<u>L14</u>
<u>L13</u>	HSP?? same arthritis	59	<u>L13</u>
<u>L12</u>	HSP?? and arthritis	350	<u>L12</u>
<u>L11</u>	L9 and (HSP70 same arthritis)	4	<u>L11</u>
<u>L10</u>	L9 and (HSP same arthritis)	1	<u>L10</u>
<u>L9</u>	L8 and @RLAD<19981008	73	<u>L9</u>
<u>L8</u>	HSP70 and arthritis	174	<u>L8</u>
<u>L7</u>	burmester-gerd-r.in.	2	<u>L7</u>
<u>L6</u>	L1 and arthritis	125	<u>L6</u>
<u>L5</u>	wehlan-helmut.in.	0	<u>L5</u>
<u>L4</u>	anti-Bip-antibodies	0	<u>L4</u>
<u>L3</u>	L1 same arthritis	1	<u>L3</u>
<u>L2</u>	L1 sme arthritis	45648	<u>L2</u>
<u>L1</u>	Bip or GRP78	1692	<u>L1</u>

END OF SEARCH HISTORY



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### GeneCard for gene **HSPA5** **GC09M119111**

Approved [UCL/HGNC/HUGO Human Gene Nomenclature database](#) symbol  
**HSPA5 (heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa))**

#### Aliases and Additional Descriptions

(According to [GDB](#), [HUGO](#),  
and/or [SWISS-PROT](#))

- BiP
- **GRP78**
- heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
- heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
- 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin hea

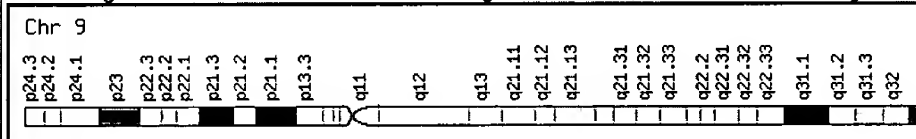
#### Chromosomal Location

(According to [UDB/GeneLoc](#)  
and/or [HUGO](#), and/or  
[LocusLink](#),  
Genomic Views According to  
[UCSC](#) and [Ensembl](#))

**Chromosome: 9** [UDB/GeneLoc gene densities](#)

**LocusLink cytogenetic band: 9q33-q34.1** **Ensembl cytogenetic band: 9q33.3**

**Gene in genomic location: bands according to Ensembl, locations according to UI**



**Unified DataBase (GeneLoc) location for GC09M119111:** (about GC identifiers)

**Start:** 119,111,854 bp from *pter*

**End:** 119,118,331 bp from *pter*

**Size:** 6,477 bases

**Orientation:** minus strand

**Unified DataBase (version 2.5) coordinate (from *pter*):** 143.335 mega bases

**Genomic View:**  
[UCSC Golden Path](#)

#### Proteins

(According to [SWISS-PROT](#)  
and/or [MIPS](#))

#### GR78 HUMAN

**Size:** 654 amino acids; 72333 Da

**Function:** PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF

**Subcellular location:** Endoplasmic reticulum lumen.

**Similarity:** BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

**MIPS Pedant Viewer:** [72428](#)

**REFSEQ proteins:** [NP\\_005338.1](#)

#### Protein Domains/Families/Ontologies

(According to [InterPro](#), [GO](#),  
and/or [BLOCKS](#))

#### InterPro Domains and Families:

[IPR001023; Hsp70](#)

[IPR000886; ER target](#)

[Graphical View of Domain Structure for SP Entry P11021](#)

#### Gene Ontology (GO) terms (tree view):

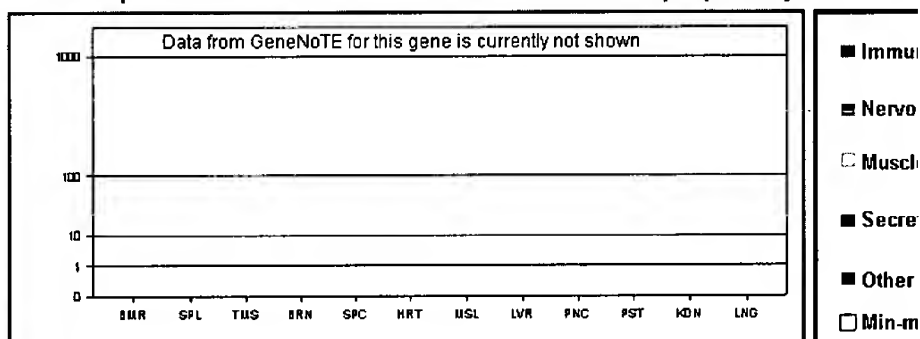
[GO:0005524](#)

GO:0008077

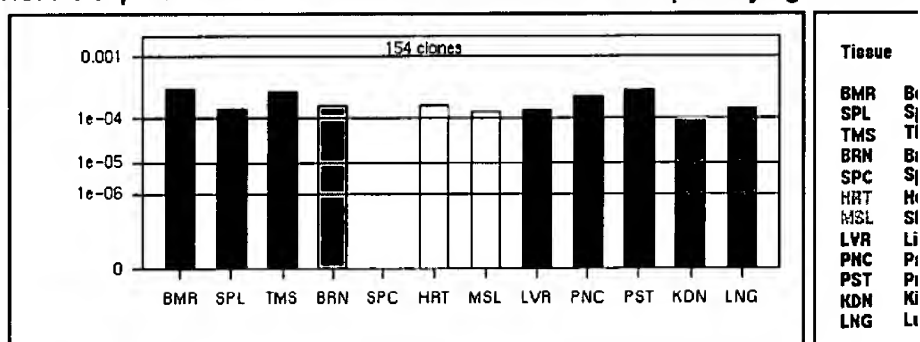
GO:0005788

**Blocks protein family:** [IPB001023](#) Heat shock protein hsp70**REFSEQ mRNAs:** [NM\\_005347.2](#)**Additional Gene/cDNA sequence:**[AF216292](#) [AF216292.1](#) [AJ271729](#) [AJ271729.1](#) [BC020235](#) [BC020235.1](#) [M15X87949.1](#)**MIPS assembly:** [H56456S1](#)**DOTS assembly:**[DT.87008863](#) [DT.91778195](#) [DT.95343265](#) [DT.97868449](#) [DT.95296185](#) [DT.95295959](#) [DT.97868444](#) [DT.40126798](#) [DT.91778226](#) [DT.95378439](#) [DT.95285344](#) [DT.95295962](#) [DT.95296183](#) [DT.97864054](#) [DT.40115805](#)**Unigene Cluster for HSPA5:** ( Build 155 Homo sapiens; Sep 23 2002 )  
heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)  
[Hs.75410](#) [\[show with all ESTs\]](#)**Unigene Representative Sequence:** [NM\\_005347](#)

**Sequences**  
(GenBank/EMBL/DDBJ  
Accessions According to  
[Unigene](#) or [GenBank](#), RefSeq  
According to [LocusLink](#),  
Assembly According to [MIPS](#)  
and/or [DOTS](#))

**HSPA5 expression in normal human tissues based on proprietary W.I.S DN**

**Expression in Human Tissues**  
(According to proprietary W.I.S  
DNA array results (GeneNoTE),  
[UniGene](#) and/or [SOURCE](#))

**HSPA5 expression in normal human tissues based on quantifying ESTs from****SOURCE GeneReport for Unigene cluster [Hs.75410](#)**

**Similar Genes in Other  
Organisms**  
(According to [MGD](#) Oct 18 2002  
, [Stony Brook](#)  
[C.elegans-H.sapiens Alignment](#)  
[Database](#) and/or [euGenes](#))

**Homologues:**

	gene	locus	description
mouse (MGD)	<a href="#">Hspa5</a>	<a href="#">2 (22.50 cM)</a>	heat shock 70kD protein 5 (glucose-regula 78kD)
<b>C. elegans</b> (Stony Brook)	<a href="#">F43E2.8</a>	--	description: Caenorhabditis elegans cosm complete sequence

<b>SNPs/Variants</b> (According to the <u>NCBI SNP Database</u> and to <u>SWISS-PROT</u> )	Variants: <u>SWISS-PROT: GR78 HUMAN</u>					
	NCBI SNPs: 8 selected, not withdrawn, single nucleotide mutations are shown here					
	<b>Genomic Data</b>					
	<b>SNP ID</b>	<b>Contig Accession</b>	<b>Position in Contig</b>	<b>Strand</b>	<b>5' Flanking Sequence*</b>	<b>3' Flanking :</b>
	<a href="#">rs12009</a>	<a href="#">NT_029366.6</a>	<a href="#">1388056</a>	-	<a href="#">AGGCCAAGCCCAATA</a>	<a href="#">AGCCATTA</a>
	<a href="#">rs7922</a>	<a href="#">NT_029366.6</a>	<a href="#">1389486</a>	-	<a href="#">CTGCTATAGCCTAAG</a>	<a href="#">GGCTGTTT</a>
	<a href="#">rs430397</a>	<a href="#">NT_029366.6</a>	<a href="#">1391872</a>	-	<a href="#">CATCACAGTAACCAT</a>	<a href="#">TCTTTTTT</a>
	<a href="#">rs387491</a>	<a href="#">NT_029366.6</a>	<a href="#">1394201</a>	+	<a href="#">CAGTCCAGCCACAGG</a>	<a href="#">CGTAGCAC</a>
	<a href="#">rs424676</a>	<a href="#">NT_029366.6</a>	<a href="#">1394200</a>	+	<a href="#">GCAGTCCAGCCACAG</a>	<a href="#">CCGTAGCA</a>
	<a href="#">rs8759</a>	<a href="#">NT_029366.6</a>	<a href="#">1389404</a>	-	<a href="#">GCCATCTTAAAAAGC</a>	<a href="#">GGTAAAAA</a>
<a href="#">rs589306</a>	<a href="#">NT_029366.6</a>	<a href="#">1392756</a>	-	<a href="#">tttttttttttt</a>	<a href="#">aattttcag</a>	
<a href="#">rs391957</a>	<a href="#">NT_029366.6</a>	<a href="#">1394777</a>	+	<a href="#">GGATCTGAAACTTTT</a>	<a href="#">CTTCTCTA</a>	
* Lower case letters indicate repetitive or low-complexity sequence						
<b>All NCBI SNPs in <u>HSPA5</u></b>						
<b>Disorders &amp; Mutations</b> (in which this Gene is Involved, According to <u>OMIM</u> , <u>SWISS-PROT</u> , <u>Genatlas</u> , <u>GeneClinics</u> , <u>HGMD</u> , <u>BCGD</u> , and/or <u>TGDB</u> .)	--					
<b>Medical News</b> (Possibly Related Articles in <u>Doctor's Guide</u> )	--					
<b>Research Articles</b> (in <u>PubMed</u> )	<ul style="list-style-type: none"><li>• <u>Human gene encoding the 78,000-dalton glucose-regulated protein and its p</u></li></ul> <div>Search PubMed for HSPA5</div> to find abstracts of <b>research articles</b>					
<b>HSPA5 in Other Genome Wide Resources:</b> (According to <u>GDB</u> , <u>LocusLink</u> , <u>euGenes</u> , <u>Ensembl</u> and/or <u>GeneLynx</u> )	<a href="#">GDB: 127962</a> <a href="#">LocusLink: 3309</a> <a href="#">euGenes: HUgn3309</a> <a href="#">Ensembl: ENSG</a>					
<b>HSPA5 in General Databases, Limited Scope</b> (According to <u>HUGE</u> )	--					
<b>HSPA5 in Specialized Databases</b> (According to <u>ATLAS</u> , <u>GENATLAS</u> , <u>HORDE</u> , <u>IMGT</u> , <u>MTDB</u> , <u>LEIDEN</u> and/or <u>SWISS-PROT</u> )	<i>name</i> <b>Genatlas</b> biochemistry entry for HSPA5: glucose regulated protein (78kDa),HSP of PPP1CC2					
<b>Services</b> (According to <u>RZPD</u> )	<a href="#">Search RZPD for clones of HSPA5</a> Clone collection at the German Human Gen					
<a href="#">Back (to Search Results)</a>	- <a href="#">More like this</a>					
<div>Search the web for HSPA5</div>	- search millions of <b>Web pages</b> with <b>Excite</b> to find other web sites relate					

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Developed at the [Crown Human Genome Center & Weizmann Institute of Science](#)

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# NiceProt View of SWISS-PROT: P11021

## General information about the entry

Entry name	<b>GR78_HUMAN</b>
Primary accession number	<b>P11021</b>
Secondary accession number	<b>Q9NPF1</b>
Entered in SWISS-PROT in	Release 11, July 1989
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, June 2002

## Name and origin of the protein

Protein name	<b>78 kDa glucose-regulated protein [Precursor]</b>
Synonyms	<b>GRP 78</b> <b>Immunoglobulin heavy chain binding protein</b> <b>BIP</b> <b>Endoplasmic reticulum lumenal Ca<sup>2+</sup> binding protein grp78</b>
Gene name	<b>HSPA5</b> or <b>GRP78</b>
From	<i>Homo sapiens</i> (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
MEDLINE=88283347; PubMed=2840249;  
Ting J., Lee A.S.;  
"Human gene encoding the 78,000-dalton glucose-regulated protein and its pseudogene: structure, conservation, and regulation.";  
DNA 7:275-286(1988).
- [2] SEQUENCE FROM NUCLEIC ACID.  
TISSUE=Cervical carcinoma;  
Chao C.C.K.;  
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
- [3] SEQUENCE FROM NUCLEIC ACID.  
TISSUE=Fibroblast;  
Hansen J.J., Nielsen M.N., Jorgensen M.M., Gregersen N., Bolund L.;  
"Grp78 is involved in the quality control of the LDL-receptor.";  
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
- [4] SEQUENCE FROM NUCLEIC ACID.  
Bermudez-Fajardo A., Llewellyn D.H., Campbell A.K., Errington R.R.;  
"Sequence differences between human grp78/BiP isolated from HeLa cells and previously reported human sequences.";  
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
- [5] SEQUENCE OF 1-25 FROM NUCLEIC ACID.  
MEDLINE=93126087; PubMed=1480470;  
Chao C.C.K., Lin-Chao S.;  
"A direct-repeat sequence of the human BiP gene is required for A23187-mediated inducibility and an inducible nuclear factor binding.";  
Nucleic Acids Res. 20:6481-6485(1992).
- [6] SEQUENCE OF 22-38.  
TISSUE=Breast carcinoma;  
MEDLINE=97295304; PubMed=9150946;  
Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E., Simpson R.J., Dorow D.S.;  
"Two-dimensional electrophoretic analysis of human breast carcinoma proteins: mapping of proteins that bind to the SH3 domain of mixed lineage kinase MLK2.";  
Electrophoresis 18:588-598(1997).
- [7] SEQUENCE OF 19-40.  
TISSUE=Colon carcinoma;  
MEDLINE=97295306; PubMed=9150948;  
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
"A two-dimensional gel database of human colon carcinoma proteins.";  
Electrophoresis 18:605-613(1997).

## Comments

- **FUNCTION:** PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
- **SUBCELLULAR LOCATION:** Endoplasmic reticulum lumen.
- **SIMILARITY:** BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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## Cross-references

EMBL	M19645; AAA52614.1; -. X87949; CAA61201.1; -. AJ271729; CAB71335.1; -. AF216292; AAF42836.1; -. X59969; CAA42595.1; -.
PIR	A29821; A29821.
HSSP	P19120; 3HSC.
SWISS-2DPAGE	P11021; HUMAN.
PMMA-2DPAGE	P11021; -.
PHCI-2DPAGE	P11021; -.
Siena-2DPAGE	P11021; -.
Genew	HGNC:5238; HSPA5.
MIM	138120 .
GeneCards	HSPA5.
GeneLynx	HSPA5; Homo sapiens.
InterPro	IPR000886; ER_target. IPR001023; Hsp70.
Pfam	PF00012; HSP70; 1.
PRINTS	PR00301; HEATSHOCK70.
ProDom	PD000089; Hsp70; 1. [Domain structure / List of seq. sharing at least 1 domain].
PROSITE	PS00014; ER_TARGET; 1. PS00297; HSP70_1; 1. PS00329; HSP70_2; 1. PS01036; HSP70_3; 1.
Implicit links to	SOURCE; Ensembl; BLOCKS; ProtoNet; ProtoMap; PRESAGE; DIP; ModBase.

## Keywords

**ATP-binding; Endoplasmic reticulum; Signal.**

## Features

Key	From	To	Length	Description
SIGNAL	1	18	18	
CHAIN	19	654	636	78 KDA GLUCOSE-REGULATED PROTEIN.
SITE	651	654	4	PREVENT SECRETION FROM ER.
CONFLICT	297	297		MISSING (IN REF. 1 AND 2).
CONFLICT	418	418		D -> H (IN REF. 1 AND 2).
CONFLICT	439	439		R -> S (IN REF. 1 AND 2).
CONFLICT	447	447		K -> N (IN REF. 1 AND 2).

## Sequence information

Length: **654 AA** [This is the length of the unprocessed precursor]  
Molecular weight: **72333 Da** [This is the MW of the unprocessed precursor]  
CRC64: **59B7D8D85BC32A00** [This is a checksum on the sequence]

10	20	30	40	50	60
MKLSLVAAML	LLLSAARAE	EDKKEDVGT	VGIDLGTYS	CVGVFKNGRV	EIIANDQGNR
70	80	90	100	110	120
ITPSYVAFTP	EGERLIGDAA	KNQLTSNPEN	TVFDAKRLIG	RTWNDPSVQQ	DIKFLPFKVV
130	140	150	160	170	180
EKKTKPYIQV	DIGGGQTKTF	APEEISAMVL	TKMKETAEAY	LGKKVTHAVV	TVPAYFNDAQ
190	200	210	220	230	240
RQATKDAGTI	AGLNVMRIIN	EPTAAAIAYG	LDKREGEKNI	LVFDLGGGTF	DVSLLTIDNG
250	260	270	280	290	300
VFEVVATNGD	THLGGEDFDQ	RVMEHFIKLY	KKKTGKDVRK	DNRAVQKLRR	EVEKAKRALS
310	320	330	340	350	360
SOHQARIEIE	SFYEGEDFSE	TLTRAKFEEL	NMDLFRSTMK	PVQKVLESD	LKKSIDEIV
370	380	390	400	410	420
LVGGSTRIPK	IQQLVKEFFN	GKEPSRGINP	DEAVAYGAAV	QAGVLSGDQD	TGDLVLLDVC
430	440	450	460	470	480
PLTLGIETVG	GVMTKLIPRN	TVVPTKKSQI	FSTASDNQPT	VTIKVYEGER	PLTKDNHLLG
490	500	510	520	530	540
TFDLTGIPPA	PRGVPQIEVT	FEIDVNGILR	VTAEDKGTGN	KNKITITNDQ	NRLTPEEIER
550	560	570	580	590	600
MVNDAEKFAE	EDKKLKERID	TRNELESYAY	SLKNQIGDKE	KLGGKLSSD	KETMEKAVEE
610	620	630	640	650	
KIEWLESHQD	ADIEDFKAKK	KELEEIVQPI	ISKLYGSAGP	PPTGEEDTAE	KDEL